

Figure 1.

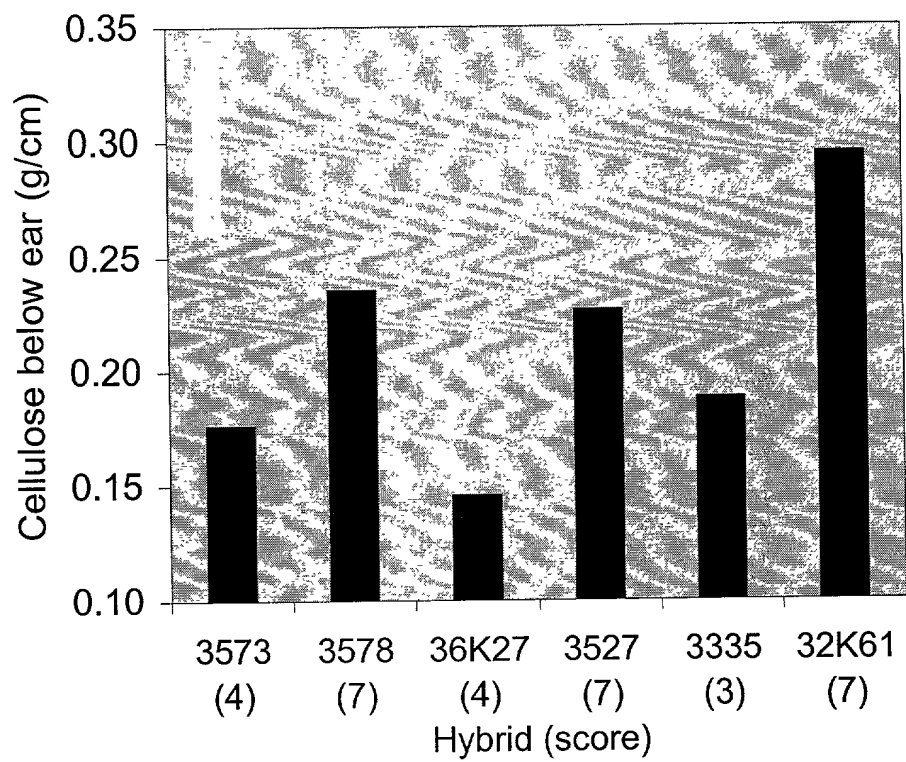


Figure 2

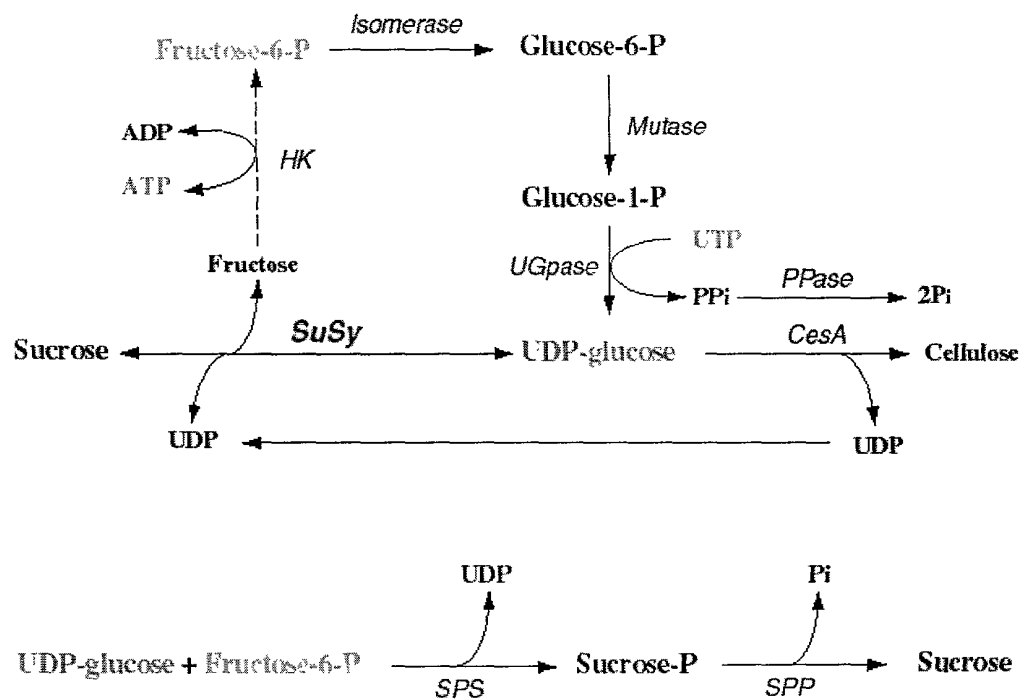


Figure 3.

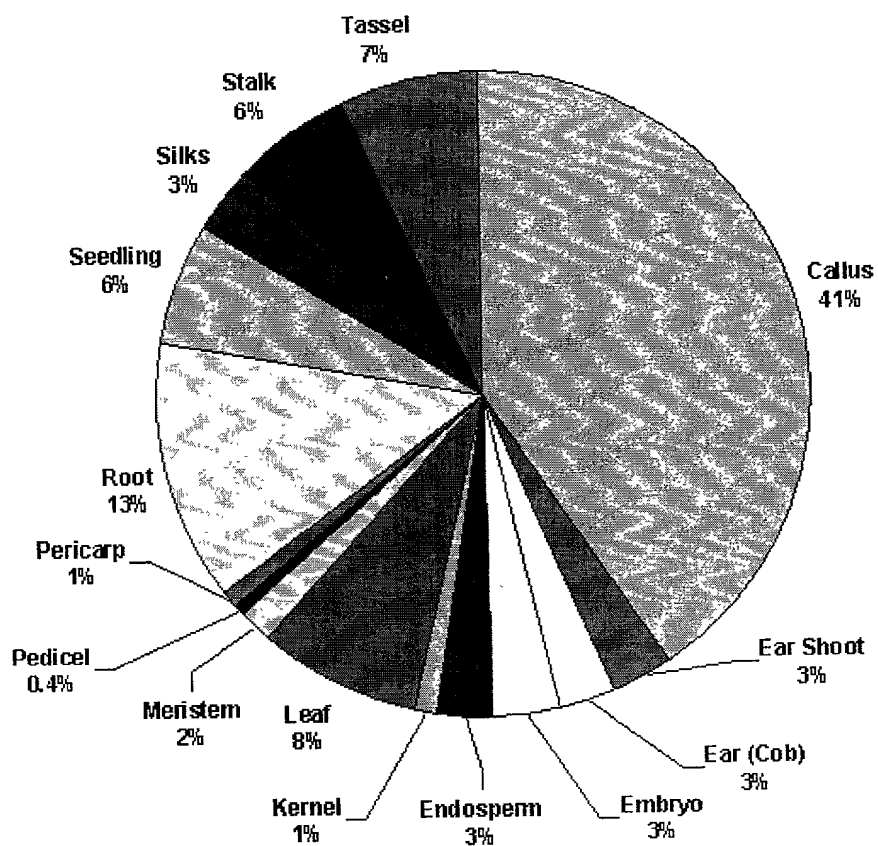


Figure 4.

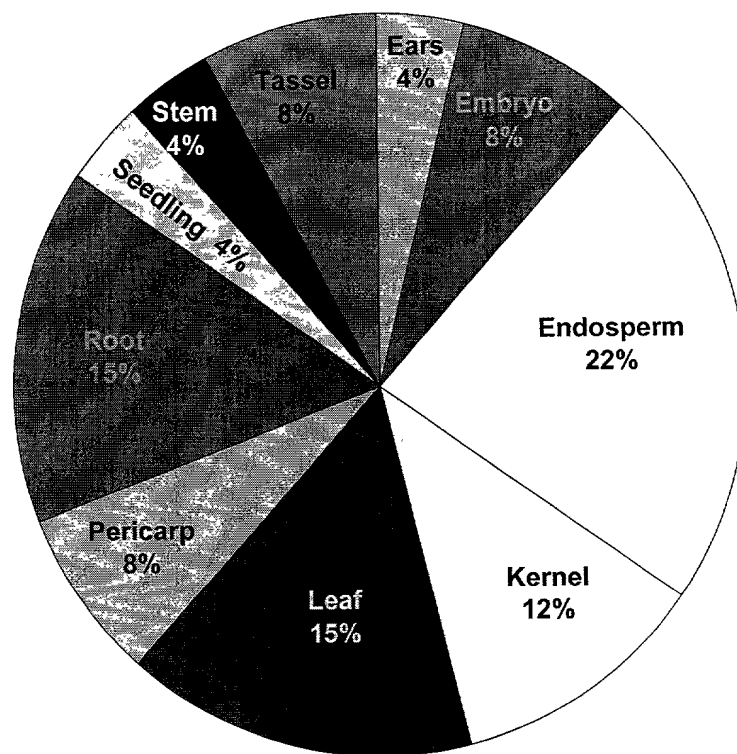


Figure 5

Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG



Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

1008014.022402

		1	50
Sh1	(1)	-----MAAKLTRLHSLRERIGATFSSHPNELIALFSRYVHQCKGMLQRHQ	
Sus1	(1)	MGEAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLCKGMLQPHQ	
Sus3	(1)	-----STHASGDRVEDTLHAHRNELVALLSKYVNKCKGILQPHH	
Consensus	(1)	LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ	
		51	100
Sh1	(46)	LLAEFD-ALFDSDE--KYAPFEDILRAAQEAIVLPWVALAIRPRPGVW	
Sus1	(51)	ILAEYNNATPEAREKLKDGAFEDVLRAAQEAIVLPWVALAIRPRPGVW	
Sus3	(40)	ILDALDEVQSGGRA-LAEGPFLVLRSAQEAIVLPWVALAVRPRPGVW	
Consensus	(51)	ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPWVALAIRPRPGVW	
		101	150
Sh1	(93)	DYIRVNVSEMAVEELSVEYLAPKEQLVDGQSNFVLELDPEFPNASFP	
Sus1	(101)	EYVRVNVSELAVEELRVPEYLQFKEQLVEGPNNNFVLELDPEFPNASFP	
Sus3	(89)	EYVRVNVHESVLEQLTVSEYLREKKEELVDGQHNDPVLVLELDPEFPNVSP	
Consensus	(101)	EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDPEFPNASFP	
		151	200
Sh1	(143)	RPSMSKSTGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTMMLN	
Sus1	(151)	RPSLSKSTGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLN	
Sus3	(139)	RPNRSSSTGNGVQFLNRHLSSIMERNRDCLEPLDFLRGHHRKHCHVMMLN	
Consensus	(151)	RPSLSKSTGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN	
		201	250
Sh1	(193)	DRIQSLRGLOSSERKAEHYLLSVPODTPYSEFNHRFOELGLEKGCWGD TAK	
Sus1	(201)	DRIRSLALQCALRKAEHLSTLQADTPYSEFHHRFOELGLEKGCWGDCAK	
Sus3	(189)	DRIQSLGRLOSVITKAEHLISKLPADTPYSQFAYKFOELGLEKGCWGD TAG	
Consensus	(201)	DRIQSL ALQSA LRKAEHLSSLPADTPYSEF HRFQELGLEKGCWGD TAK	
		251	300
Sh1	(243)	RVLDTLHLILLDLLEAPDPANLEKFLGTIPMFMNVVILSPHGYFAQSNVLG	
Sus1	(251)	RAQETIHLILLDLLEAPDPSTLEKFLGTIPMFMNVVILSPHGYFAQANVLG	
Sus3	(239)	HVLEMIHLILLDLIQAPDPSTLEKFLGTIPMFMNVVWVSPHGYFQAQANVLG	
Consensus	(251)	RVLETIHLILLDLLEAPDPSTLEKFLGTIPMFMNVVILSPHGYFAQANVLG	
		301	350
Sh1	(293)	YPDTCGQVVYILDQVRALENEMLLRIKQOGLDITPKILIVRLLPDAAGT	
Sus1	(301)	YPDTCGQVVYILDQVRAMENEMLLRIKQOGLDITPKILIVRLLPDATST	
Sus3	(289)	LPDTCGQVVYILDQVRALENEMVLRKKOGLDVSPKILIVRLLPDAKGT	
Consensus	(301)	YPDTCGQVVYILDQVRALENEMLLRIKQOGLDITPKILIVTRLLPDA GT	
		351	400
Sh1	(343)	TCGQRLKVKVTCETHDLRVVFRNENGILRKWISRFDVWPYLETYTEDVS	
Sus1	(351)	TCGQRLKVKVIGTEHCHILRVVFRTENGIVRKWISRFVWPYLETYTDEVA	
Sus3	(339)	SCNQRLERISGTOHTYLLRVVFRNENGILKKWISRFDVWPYLETFEADAA	
Consensus	(351)	TCGQRLKVKVIGTEHTHILRVVFRNENGILRKWISRFDVWPYLETYTEDVA	
		401	450
Sh1	(393)	SEIMKEMQAKPDLIIGNYSDGNLVATLAAHLGVTOCTIAHALEKTKYPN	
Sus1	(401)	HEIAGELQANPDITIGNYSDGNLVACLLAHKMCVTHCTIAHALEKTKYPN	
Sus3	(389)	GEIAAELQCTPDTIGNYSDGNLVASLLSYKMGITOCNIAHALEKTKYPD	
Consensus	(401)	EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN	
		451	500
Sh1	(443)	SDIYLCKEDSQYHESCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGOYE	
Sus1	(451)	SDIYWKKFEDHYHESCQFTDLIAMNHADFIITSTFQEIACNKDTVGOYE	
Sus3	(439)	SDIFWKNFDEKYHESCQFTADLIAMNADFIITSTYQEIAGSKNTVGOYE	
Consensus	(451)	SDIYWKKFDD YHESCQFTADLIAMNHADFIITSTFQEIAGSKDTVGOYE	
		501	550
Sh1	(493)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTESKRLTSLH	
Sus1	(501)	SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH	
Sus3	(489)	SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTKAKRLTSLH	
Consensus	(501)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH	

Figure 8a

		551		600
Sh1	(543)	PEIEELIYSDVENSEHKFVLKDKKKPTIESMARLDRVKNMTGLVEMYGKN		
Sus1	(551)	PEIEELIYSOTENTSHKFVLNDRNKPTIFSMARLDRVKNITGLVETLYGRN		
Sus3	(539)	GSIENLIYDPEONDEHIGHLDDRSKPTIFSMARLDRVKNITGLVEAFKAC		
Consensus	(551)	PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN		
		601		650
Sh1	(593)	ARRELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWTS		
Sus1	(601)	KRLOELVNLVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWTS		
Sus3	(589)	AKLRELVLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFQOFRWIS		
Consensus	(601)	ARLRELVLVVVAGDHG SKDREEQAEFKKMHDLDLID YNL GHIRWIS		
		651		700
Sh1	(642)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAAGLTVLESMTCCGLPTIATCH		
Sus1	(650)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAAGLTVVEAMTCGLPTFATAY		
Sus3	(639)	AQTNRARNGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLH		
Consensus	(651)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAAGLTVVEAMTCGLPTFAT H		
		701		750
Sh1	(692)	GGPAETIVDGVSGLHIDPYHSDKAADILVNFEKCKADESYWDEISQGGL		
Sus1	(700)	GGPAETIVHGVSCYHIDPYQGDKASALLVDFFDKCAEESHESKISQGGL		
Sus3	(689)	GGPAETIEHCVSCHIDPYHPEQAVNLMADEFDRCQODEDHVNVNISGAGL		
Consensus	(701)	GGPAETIVHGVSGFHIDPYH DKAALVDFFDKCKADPSHW ISQGGL		
		751		800
Sh1	(742)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR		
Sus1	(750)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR		
Sus3	(739)	QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR		
Consensus	(751)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR		
		801		817
Sh1	(792)	SLASQVPLSFD-----		
Sus1	(800)	IMASTVPLAVEGEPSSK		
Sus3	(789)	ELAKTVPLAID-QPQ--		
Consensus	(801)	SLASTVPLAID P		

Figure 8b

		1	50
Sh1	(1)	AAACCCTCCCTCCCTCCTCCATTGGACTGCTTGCTCCCTGTTGACCAATTG	
Sus1	(1)	-----GCCTGAG-GATCCAGGAAGAGGACAG	
Sus3	(1)	-----	
Consensus	(1)	G CTG G TCC G GA A G	
		51	100
Sh1	(51)	GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCCCTTTCACAG	
Sus1	(26)	CA-ATGGGGGAAGGTGCAGGTGACCGTGTCTCTGAGCCGCTCCACAG	
Sus3	(1)	-----CTCCGAC-CCAGGC	
Consensus	(51)	AT G A T AG TG C CTGAGTCGCCTCCACAG	
		101	150
Sh1	(101)	TCTTCGGGAACGGCTTGGTGCCACCTTCTCCTCCCATCCCAATGAACCTGA	
Sus1	(72)	CGTCAGGGAGCGGATTGGCGAGTCACTCTCTGCCACCCCAATGAGCTTG	
Sus3	(13)	GTCCGGCGACCGCGTCCAGGACACCCCTCCACGCGGACCGCAACGAGCTCG	
Consensus	(101)	TC GCGA CGC TTGG GACACCCTCTCCGCCACCCCAATGAGCT G	
		151	200
Sh1	(151)	TAGCACTCTTTTCCAGGTATGTTCAACAGGGCAAGGGAATGCTTCAGCGC	
Sus1	(122)	TGGCGCTCTTCACCAGGCTGAAAAACCTTGGAAAGGGTATGCTGCAGCGC	
Sus3	(63)	TGGCGCTCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCTGCAGCGC	
Consensus	(151)	TGGCGCTCTT TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC	
		201	250
Sh1	(201)	CATCAGCTGCTTCGGCAGTTTGA---TGC---CCTGTT--TGATAGTGA	
Sus1	(172)	CACCAGATCATTCGGGAGTAAACAATGCGATCCCTGAGCCTCAGCGCGA	
Sus3	(113)	CACCACATCTTCGACGCTTCGACGAGGT---CCAGGG-CTCCGGGGGC	
Consensus	(201)	CACCAGATCCTTGCCGAGTTCGAC ATGC CCTG G CTGAG G GA	
		251	300
Sh1	(242)	CAAGGAGAAG--TATGCACCAATTGAAGACATTCCTCGTCTCCTCAGGA	
Sus1	(222)	GAAGCTCAAG--GATCGTGCTTTGAGCATGTCCTGAGGGCAGCTCAGGA	
Sus3	(158)	CGCGCGTAGCCGAGGGACCTTCCTCGACGTCTCTCGCTCCGCGCAGGA	
Consensus	(251)	CAAGC CAAG GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA	
		301	350
Sh1	(290)	AGCAATTGTGCTCCCCCATGGGTGCACTTGCTATCAGGCGAAGGCCTG	
Sus1	(270)	GGCGATTCTCATCCCCCATGGGTGCACTTGCCATCCGCGCTAGGGCTG	
Sus3	(208)	GGCGATTCTGCTGCGCGGTTCTGTTGCCATCGGGTGGCGCCGCGCCCGG	
Consensus	(301)	GGCGATTGTGCTCCCCCATGGGTGCACTTGC ATCCGCC AGGCCTG	
		351	400
Sh1	(340)	GTCCTGCGCATTACATTCGGGTGAATGTAAGTGAGCTGGCTGTGAGGAG	
Sus1	(320)	GTCTCTCCGAGTATGAGGGTCAACGTCAGTCAGCTCGCTGTGAGGAG	
Sus3	(258)	GAGTTTGGGAGTACGTCCGCGTCAACGTCACGAGCTCAGCTTCGAGCAG	
Consensus	(351)	GTGTCTGGGAGTACGT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG	
		401	450
Sh1	(390)	CTGAGTGTCTTCTGACTACTTGGCATTCAAGCAACAGCTGCTGGATGGACA	
Sus1	(370)	CTGAGACTTCCTGAGTACCTGCAGTTCAGCAACAGCTTGTGGAAGGAGG	
Sus3	(308)	CTCAGACTCTCGGAGTACCTCCGCTTCAGGAGGAGCTTGTGACCGCCA	
Consensus	(401)	CTGAGAGTTTCTGAGTACCTGC TTCAAGGAACAGCTTGTGGA GGACA	
		451	500
Sh1	(440)	ATCCAACAGCAACTTGTGCTTCAGCTTGATTTTACGCCCTTCAATGCCT	
Sus1	(420)	CCCAACAACAACCTTGTCTTTGAGCTGGACTTTGAGCCATTCAATGCCT	
Sus3	(358)	GCACAATGATCCCTACCTTCTCCAGCTTGACTTCGAGCCGTTCAATGTCT	
Consensus	(451)	CCCAACAACAACCTTGTCTTTGAGCTTGACTTTGAGCC TTCAATGCCT	
		501	550
Sh1	(490)	CCTTTCCTCGTCTTCCATGTGCAAGTCCATCGCAAAATGGAGTGAATTC	
Sus1	(470)	CCTTCCCCTGCTCTTCTCTGTCAAAGTCCATTGGCAATGGCGTGCAGTTC	
Sus3	(408)	CAGTCCACGCCCCAAATCCGTCATCATCTATTGCAAAACGGTGTGCAGTTC	
Consensus	(501)	CCTTCCC CGTCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC	

Figure 9a

		551	600
Sh1	(540)	CTTAACCGACACCTGTCCTCAAGTTGTTCCAGGACAAGGAGAGTTTCTA	
Sus1	(520)	CTCAACAGGCACCTGTCAATCAAAGCTCTTCCATGACAAGGAGAGCATGTA	
Sus3	(458)	CTCAACCGACACCTTGTCTCAATCATGTTCCGCAACAGGCATTGCTTGA	
Consensus	(551)	CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGT	
		601	650
Sh1	(590)	CCCCCTTGTGAAGTTCTCTCAAGGCTCATAACTACAAGCGCAGGACGATGA	
Sus1	(570)	CCCCCTTCTCAACTTCTCTTCCGCCCACAAGTACAAGGGGATCACCATGA	
Sus3	(508)	CCCCCTGTTGGATTCTCTCCGTGCCACCGGCACAAGGGGCATGTTATGA	
Consensus	(601)	CCCCCTTGTGAAGTTCTCTCCG GCCACAAGTACAAGGGGA GAC ATGA	
		651	700
Sh1	(640)	TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCTTGAGA	
Sus1	(620)	TGTTGAATGACAGAATCCGCACTCTCAAGGCTTGGGCTGAGG	
Sus3	(558)	TGCTTAATGATAGAATAAAGCTTGGGGAGGCTTCACTCTGTGCTGACC	
Consensus	(651)	TGTTGAATGACAGAATCCAAAGCCT GTGGTCT CAATCTGCGCTGAG	
		701	750
Sh1	(690)	AAGGCTGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
Sus1	(670)	AAGGCTGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
Sus3	(608)	AAGGCTGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
Consensus	(701)	AAGGCTGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
		751	800
Sh1	(740)	GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGTTGGGGTGACA	
Sus1	(720)	ATTTACCCACAGGTTCCAGGAATTCCTCTGGAGAAGGTTGGGGTGATT	
Sus3	(658)	ATTTGCTTATAAATTTCAAGAGTGGGGCTGGAGAAAGCTTGGGGTGATA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGTTGGGGTGATA	
		801	850
Sh1	(790)	CTGCGAAGCTGTTCTCCACACACTCCACTTGTCTTCTGACCTTCTTGAG	
Sus1	(770)	GCGCTAAGCTGTCACAGGAGTATCCACCTTCTCTTGACCTCTCTGAG	
Sus3	(708)	CAGCAGGACATGTTTGGAAATGATCCATCTCTCTTAGACATCATTCAG	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCCTTCT GACCTCTTGAG	
		851	900
Sh1	(840)	CCCCCTCATCTGCCAAGTTGGAGAAGTTCCCTTGGAACTATACGAATGAT	
Sus1	(820)	CCCCCAGATCCGTCACCCCTGGAGAAGTTCCCTTGGAAAGATCCCCATGAT	
Sus3	(758)	CCCCCAGATCCGTCACCCCTAGAGAAATTTCTTGGGAGGATCCCCATGAT	
Consensus	(851)	GCCCCAGATCC TCCACCTGGAGAAGTTCCCTTGGAAAGATCCCCATGAT	
		901	950
Sh1	(890)	GTTCAACGTTGTTATCTCTGCTCTCATGGCTACTTGGCCAGTCCAATG	
Sus1	(870)	GTTCAACGTTGTTATCTCTCTCATGGCTACTTGGCTCAAGCTAATG	
Sus3	(808)	TTTTAACGTTGTTGCTATCCCTCATGGATAGTTTGGTCAAGCTAATG	
Consensus	(901)	GTTCAACGTTGTTATCT TCCCCTCATGG TACTTGGCTCAAGCTAATG	
		951	1000
Sh1	(940)	TGCTTCCAATACCTTCACACTGGCGGTCAAGTTCTGTACATCTGGATCAA	
Sus1	(920)	TCTTGGGTTACCTTGACACCGGAGGCCAGGTTGTCTACATCTTGATCAA	
Sus3	(858)	TATTAGGCTTGGCAGACACAGGAGAGATCTCTATATACTGGACCAA	
Consensus	(951)	T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA	
		1001	1050
Sh1	(990)	GTCCGTGCTTTGGAGAATCAGATGCTTCTGAGGATTAAGCAGCAAGGCT	
Sus1	(970)	GTGGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGCTCT	
Sus3	(908)	GTCCGTGCTTACAAATCAGATGCTTCTCCGTTTAAAGAAACAGGCT	
Consensus	(1001)	GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT	
		1051	1100
Sh1	(1040)	TGATATCACCTCGAAGATCCTCATTTGTTACCAGGCTGTTGCCTGATGCTG	
Sus1	(1020)	TGATATCACCTCGAAGATCCTTATTGTCAGGAGGTTGCTCCGTCATGCAA	
Sus3	(958)	TGATGTTTCCCAAGATTTCTCATTTGTTACTCGGCTGATACCAGATGCAA	
Consensus	(1051)	TGATATCAC CCGAAGATCCTCATTTGTTACCAGGCTG T CCTGATGCAA	

Figure 9b

		1101		1150
Sh1	(1090)	CTGGCAGTACGTCCGGTACCGGCTGCAGAAGGTCATTGGTACTGAGCAG		
Sus1	(1070)	CTGGCACCAGCTGTGGCCAGCCCTTGAGAAGGTCCTTGGCACCAGAC		
Sus3	(1008)	AAGGAACATCATGCAATCAGCGGCTTGAGAGAACTAGTGAACACAGCAT		
Consensus	(1101)	CTGG AC AC TGCGGTACGCGGCTTGAGAAGGTCATTGG AC GAGCAC		
		1151		1200
Sh1	(1140)	ACAGACATCATTCCGGTTCCTTCAGAAATGAGATGGCATCCTCCGCAA		
Sus1	(1120)	TGCCATATCCCTCCGGTGGCATTGAGAACAGAAACCGAATCGTTCGCAA		
Sus3	(1058)	ACTTACATATTACGACTCCCTTCAGAAATGAAATGGGATACTTAAGAA		
Consensus	(1151)	AC ACATC TTCGGTTCCTTCAGAAATGAAATGG ATCCTTCGCAA		
		1201		1250
Sh1	(1190)	GTGGATCTCTCGTTTTCATGCTCGCCATACCTGGAGACATACACTGAGG		
Sus1	(1170)	GTGGATCTCGCCATTGGAAGCTCGCCGTACCTGGAGACTTACACTGATG		
Sus3	(1108)	ATGGATATCAAGATTGATGTGCGCCATATCTGGAAACATTGCTCAGG		
Consensus	(1201)	GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG		
		1251		1300
Sh1	(1240)	ATGTTTCCAGTGAAATAATGAAAGAAATGCAGGGCAAGCCTGACCTTATC		
Sus1	(1220)	ACGTGGCGCATCAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC		
Sus3	(1158)	ATGCTGCTGCTCAAAATTCCTGCTCAATTACAAGGTATCCAGACTTCATA		
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC		
		1301		1350
Sh1	(1290)	ATTGGCAACTACAGCGATGGCAACCTAATCGGCCACTCTGCTCGGGCAGAA		
Sus1	(1270)	ATCGGAAACTACAGTACCGGAAACCTTGTTGCGTGTTCGCTCGCCACAA		
Sus3	(1208)	ATTGCAAACTACACTGATGGAATCTTCTGGCGTCATTGCTATCTTACAA		
Consensus	(1301)	ATTGGAAACTACAGTATGGAACCTTGT GCGTCTTTGCTCGC CACAA		
		1351		1400
Sh1	(1340)	GTTCGGAGTCACTCAGTCTACCATCGCTCAAGCCTTGAGAAAACCAAA		
Sus1	(1320)	CATGGCTGTACTCACTGTACCATTCCTCATGGCTTCAGAAAACCTAAGT		
Sus3	(1258)	GATGGCAATTACCAAGTCAACATTCCTCATGCTCTGCAAAAGACTAAGT		
Consensus	(1351)	GATGGGAGTTACTCAGTGTACCATGTCTCATGC CTGGAGAAAACCTAAGT		
		1401		1450
Sh1	(1390)	ACCCCAACTCGCAATCTACTTGGCAAAATTCGACAGCCAGTACCACTTC		
Sus1	(1370)	ACCGTAACCTCCAGCTCTACTGGAAGAGTTTGAGGATCACTACCACTTC		
Sus3	(1308)	ATGCAGATTACACATATTTTGAAGAAATTCGATGAGAAGTACCATTC		
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC		
		1451		1500
Sh1	(1440)	TCTTGGCAGTTACAGCTGACCTTATTGCCATGAACACACCGATTTCAT		
Sus1	(1420)	TGGTGGCAGTTACCACTGACTTGATTGCAATGAACCATGCCAGTTTCAT		
Sus3	(1358)	TCTTGGCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT		
Consensus	(1451)	TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTTCAT		
		1501		1550
Sh1	(1490)	CATCACCAGCACATTCCAAGAAATCGCGGAAGCAAGGACACCGTGGGGG		
Sus1	(1470)	CATCACCAGTACCTTCCAAGAGACCGCCGAAACAAGGACACCGTCCGGCC		
Sus3	(1408)	CATCACCAGCACATCCAAGAAATTCCTGGAAGCAAAAATAGTGTGGAC		
Consensus	(1501)	CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C		
		1551		1600
Sh1	(1540)	AGTACGAGTCCCATATCGCGTCACTCTTCTGGGCTCTACCGTCTCGTC		
Sus1	(1520)	AGTACGAGTCAACATGCGGTTCACAATGCTTGGCCTGTACCGCTTGTC		
Sus3	(1458)	AGTATGAGAGTCACTCTGCTTTACTCTGCCTGGTCTGTACCGAGTTGTC		
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC		
		1601		1650
Sh1	(1590)	CATGGCATCCATGTTTCCATCCCAAGTTCAACATTGCTCTCTCTGGAGC		
Sus1	(1570)	CACGGCATTCATGCTTCCACCCCAAGTTCAACATCGTGCTCTCTGGCGC		
Sus3	(1508)	CATGGGATCCATGCTTCCATCCCAAGTTCAATATAGTCTCTCTCTGGAGC		
Consensus	(1601)	CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCTCTGGAGC		

Figure 9c

		1651		1700
Sh1	(1640)	AGACATGAGTGTCTTACTACCGTTATACGGAAACCGACAAGAGACTCACCTG		
Sus1	(1620)	GGACCTGTGCATCTACTTCCCGTACACCGAGTCGCACAAGAGGCTGACCT		
Sus3	(1558)	TGACATGTCCATATACTTTCCACATACCGAGAAGGCCAAGCCACTCACCT		
Consensus	(1651)	GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT		
		1701		1750
Sh1	(1690)	CCTTCATCCTGAAATCCAGGAGCTCATCTACAGCGACGTCGAGAACTCC		
Sus1	(1670)	CCCTTCACCCGAGATTGAGGAGCTCTGTACAGCCAAACCGAGAACAGG		
Sus3	(1608)	CTCTTCATGGTTCAATCCGAAATTTGATTTATGACCCGAGCAAAACGAT		
Consensus	(1701)	CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C		
		1751		1800
Sh1	(1740)	GAGCACAAGTTCTGCTCAAGGACAAACAAGCCGATCATCTTCTCCAT		
Sus1	(1720)	GAGCACAAGTTCTGCTTCTCAACGACAGGAACAAGCCAATCATCTTCTCCAT		
Sus3	(1658)	CAACACATTGGGCATCTGCGATGACCGTCAAAGCCCATCTCTTCTCCAT		
Consensus	(1751)	GAGCACAAGTTCTGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT		
		1801		1850
Sh1	(1790)	GGCGCTCTCGACCCCGTGAAGAACATGACAGGCGTGGTCGAGATGTACG		
Sus1	(1770)	GGCTCGTCTCGACCGTGTGAACAACCTGACTGGCTGCTGGAGCTGTACG		
Sus3	(1708)	GGCAAGACTCGAGCGGTGAACAACATAACACCGCTGCTCGAAGCTTTTG		
Consensus	(1801)	GGC CGTCTCGACCG GTGAAGAACATGACAGGCGTGGTCGAG TGTACG		
		1851		1900
Sh1	(1840)	GCAAGAACGCGCGCTCAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT		
Sus1	(1820)	GCCGGAACAAGCGGCTCAGGAGCTGGTGAACCTCGTGGTCTGTGCGGC		
Sus3	(1758)	CTAAGTGCGCTAAGCTGAGGAGCTGGTAAGCTTGTCTGCTTGCCTGGG		
Consensus	(1851)	GCAAGAACGCGCGCTGAGGGAGCTGGTGAACCTCGTGGTCTGTGCCGG		
		1901		1950
Sh1	(1890)	GACCACGG---CAAGGAGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA		
Sus1	(1870)	GACCATCG---CAAGCCTTCCAAGGACAGGAGGAGCAGGCGGAGTTCAA		
Sus3	(1808)	TGAATGATGTCAACAAGTCCAAGGACAGGGAAGAGATCGCGGAGATAGA		
Consensus	(1901)	GACCATGG CAAC AGTCCAAGGACAGGAGGAGCAGGCGGAGTTCAA		
		1951		2000
Sh1	(1937)	GAAGATGTACAGCCTCATCGACGAGTACAACTTGAAGGCGCATATCCGGT		
Sus1	(1917)	GAAGATGTTTGACCTCATCGAGCAGTACAACTGAACGGGACATCCGGT		
Sus3	(1858)	GAAGATGCATGAACCTCATGAAGACCCACAACCTTGTTCGCGAGTTCCGGT		
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGGT		
		2001		2050
Sh1	(1987)	GGATCTCGCGGAGATGAACCGTGTCCGCAACGGCGAGCTGTACCGCTAC		
Sus1	(1967)	GGATCTCCGCCAGATGAACCGCGTCCGCAACGGCGAGCTGTACCGCTAC		
Sus3	(1908)	GGATCTCTGCCAGCAAAACAGGGCCCTAACCAGGAGCTTATCGCTAC		
Consensus	(2001)	GGATCTC GCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC		
		2051		2100
Sh1	(2037)	ATTTCGATACCAAGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT		
Sus1	(2017)	ATCTGCCACACCAAGGCGCTTCGTGCAGCCTGCTTTCTACGAGGTTT		
Sus3	(1958)	ATCGCTGATACCCATCTGCTTTGCTACAGCGCGCTTGTATGAAGCGTT		
Consensus	(2051)	ATCTGCCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT		
		2101		2150
Sh1	(2087)	CGGCCTGAGTGTGATCCAGTCCATGACGTGCGGTCTGCCAAGGATCGCGA		
Sus1	(2067)	CGGGCTGACGGTGGTTCAAGCCAACACCTGCGGCTGCCACAGTTCCGCA		
Sus3	(2008)	CGGTCTCACCGTCTGTTAGGCCATGACCTGTGGGTTCCTACTTTCGCGA		
Consensus	(2101)	CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCCGGA		
		2151		2200
Sh1	(2137)	CCTGCCATCGCCGCCCTCTGAGATCATGTGGACGGGGTATCTGGCTTG		
Sus1	(2117)	CGGCTTACGCGCGGTCCGCGAGATCATGTCACCGCGGTGTCTGGCTAC		
Sus3	(2058)	CGCTCCATCGAGGTCCAGCTGAGATCATAGCACTCGCGTCTCGGCTTC		
Consensus	(2151)	CC CCATGGCGGTCC GCTGAGATCATGTGCACGGCGT TCTGGCTTC		

Figure 9d

		2201		2250
Sh1	(2187)	CACATTGACCCCTTACCACAGCCAGAACCCCGGGATATCCTGGTCAACTT		
Sus1	(2167)	CACATCGACCCCTTACCAGGGGCGACAGCCGTCGGCCCTGCTCGTGGACTT		
Sus3	(2108)	CACATTGACCCGTAACCAACCCGACAGGCTGTTAATCTGATGGCCGACTT		
Consensus	(2201)	CACATTGACCCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTCGACTT		
		2251		2300
Sh1	(2237)	CTTTCACAAATGCAAGGCAGATCCGAGCTACTGGGACGAGATCTACAGG		
Sus1	(2217)	CTTCGACAAGTCCGAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCAGG		
Sus3	(2158)	CTTCGAGCGGTGCAAGCAAGACCCAGATCACTGGCTCAATATATCTGGAG		
Consensus	(2251)	CTTCGACAAGTGAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG		
		2301		2350
Sh1	(2287)	GCGGCCGACAGACAATTTATGAGAAGTACACCTGGAAGCTCTACTCCGAG		
Sus1	(2267)	GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGGAAGCTGTACTCGGAG		
Sus3	(2208)	CAGGGCTGCAGGCGATATACGAGAAGTACACATGGAAGATATACTACAG		
Consensus	(2301)	GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG		
		2351		2400
Sh1	(2337)	AGGCTGATGACCCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGAGCAA		
Sus1	(2317)	AGGCTGATGACCCCTCACCGGCGTGTACCGGTTCTGGAAGTACGTGTCCAA		
Sus3	(2258)	AGGCTGATGACACTGGCCGCGGCTCTACCGTTTCTGGAAGTACGTGTCCAA		
Consensus	(2351)	AGGCTGATGACCCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA		
		2401		2450
Sh1	(2387)	CCTGGAGAGCGCGGAGAACCCGCGCTACATCGAGATGTTCTACCGCCCTGA		
Sus1	(2367)	CCTGGAGAGCGCGGAGAACCCGCGCTACCTGGAGATGCTCTACCGGCTCA		
Sus3	(2308)	GCTCGAGAGCGCTGGAGAGGAGCGCTACCTTGAGATGTTCTACATACTGA		
Consensus	(2401)	CCTGGAGAGGCGCGAGAACCCGCGCTACCT GAGATGTTCTACGC CTGA		
		2451		2500
Sh1	(2437)	AGTACCGTAGCCCTGCGAAGCCAGGTTCCGCTGTCTCTCCA-----TTAG		
Sus1	(2417)	AGTACCGTAGCATGCGGAGCACCGTCCGCTCGCCCTGCA-----GGGA		
Sus3	(2358)	AGTACCGTAGCTGGCGAAGACCGTCCGCTTGAATTTACCAACCCAG		
Consensus	(2451)	AGTACCGCA CCTGGCGAGCACCGTCCGCTGGCC T GA G AG		
		2501		2550
Sh1	(2481)	TACGGGGAAAGAACGAGA-AGAAGAACAGAACCCAGGCGGA-----G		
Sus1	(2461)	GAGCCCTCCAGCAAGTGA-TCCGTGACGGCGGCCACAGACCTCATC---G		
Sus3	(2408)	TAGCTTGGCAACTGCCACTGCCGTAGCACTTGGTACAGACTGAACCTG		
Consensus	(2501)	TAGC GC AGAA G GA TGCATAACA GGCACAGGCTGA G		
		2551		2600
Sh1	(2525)	AACCATCGCTGCAATTTCCATCT-----GT-TTACCCGAATTCGC		
Sus1	(2507)	ATCCATGAGGAGAGGGAGCACTCGGA-----GT-CTCGTGTCTTTCC		
Sus3	(2458)	AAGACCTTCAATAATTTAGGCGCGGAGACGCTAGCCCAATAAAATGTGC		
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTGCG		
		2601		2650
Sh1	(2565)	ATTGTTAGTGGTGTATTGGAGTTATGTG--TACTTGGTTTCCAGAACTT		
Sus1	(2551)	TTGCCATTTCTTCTTCTCTCTTTTTC--TTCCCGAGGCGAAAAAAA		
Sus3	(2508)	CGGAGCTGAAGTCTTTTATTATGTACATAATGGCAGTATACAAAT		
Consensus	(2601)	TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT		
		2651		2700
Sh1	(2613)	TGGTTCTTCTCGTTTCTTTCTTCTTTGAGGCTTTTGGGACGCGTG		
Sus1	(2599)	AGAGTC-TGCTT-TGCTAGGCGGCGGGCTTCGTTGCTGCTCTTTGCTT		
Sus3	(2558)	TACTGAAGGACAGGTGGGTGACAGTTGTGTCTTCGTTACTG-----TT		
Consensus	(2651)	TG TTC TGCT GTTG TTG CGTTGTGTGTTCTGTT CTG C GCTT		
		2701		2750
Sh1	(2663)	GCTTCTTCTAGTATGCTGGCAATTGGCTGCACCTTTTGCTTCAATAA		
Sus1	(2647)	CAAGAGTTAAATTTACCTACC--TTGTCAAGGTCTTGTTCATCATTTGA		
Sus3	(2600)	TACTGTATTATGTCAAGCTGTG---GGCTGCAATTTCTTTGCTG--CA		
Consensus	(2701)	ACTGGTT ATATTAAGCTG C TTGGCTGCA CTT TTC TGA T A		

Figure 9e

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2751                                     2800
Sh1 (2713) AAATGCCTGCTCGTTTACCTGCTTCCAGAGTGC-----
Sus1 (2695) TCCGGGTCTCGCTTGTAGTACTCTGATGCACTGTTAGTAGTTTGCCTTGC
Sus3 (2644) AGCCGCAGGGCACTGGTGAAGTGGTGATAAATACATCATATTCTGTTGACC
Consensus (2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C
2801                                     2850
Sh1 (2747) -----
Sus1 (2745) GTCGGTTGACAGGGAACGTTGGTGGTGGTGTGTGTGTCAGTCAGGCGT
Sus3 (2694) TGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCCGC-----
Consensus (2801) G A A AA G G G C

2851                                     2900
Sh1 (2747) -----
Sus1 (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
Sus3 (2738) -----
Consensus (2851)

2901                                     2950
Sh1 (2747) -----
Sus1 (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
Sus3 (2738) -----
Consensus (2901)

2951                                     2964
Sh1 (2747) -----
Sus1 (2895) ACCTTTGCAGCTGT
Sus3 (2738) -----
Consensus (2951)

```

Figure 9f

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CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG
CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCCATGCTGCCCCGAAGCTGA
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA
TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT
TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11
 ATGTCTGCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

gtcgacccac	gcgtccggg	accgcgtcga	ggacacccctc	cacgcgcacc	gcaacgagct	60
cgctgccctc	ctgtccaagt	acgtgaacaa	ggggaagggc	atcctgcagc	cgcaccacat	120
cctcgacgcg	ctcgacgagg	tccagggctc	cggggggccg	gcgctagccg	agggaccctt	180
cctcgacgctc	ctccgctccg	cgcaggaggc	gatcgtgctg	ccgccgttcg	tggccatcgc	240
ggtgcgcccc	cgcccgggag	tttgggagta	cgcccgctc	aacgttcacg	agctcagcgt	300
cgagcagctc	acagtctcgg	agtacctccg	cttcaaggag	gagcttgctg	acggccagca	360
caatgatccc	tacgtttctg	agcttgactt	cgagccgttc	aatgtctcag	tcccacgccc	420
aaatcggtca	tcatctattg	gaaacggtgt	gcagttccctc	aaccgacact	tgctcctcaat	480
catgtttccg	aacagggatt	gcttgaggcc	cctgttggtg	ttcctccgtg	gccaccggca	540
caaggggcat	gttatgatgc	ttaatgatag	aatacaaaag	ttggggaggc	ttcagtctgt	600
gctgaccaaa	gctgaggagc	acttggtcaaa	gctccctgct	gacacacccat	actcacaatt	660
tgcttataaa	tttcaagagt	ggggcctgga	gaaaggttgg	ggtgatacag	caggacatgt	720
tttggaatag	atccatctcc	ttctagacat	cattcaggcg	ccagacccat	ctaccctaga	780
gaaattcttg	gggaggatcc	ccatgatttt	taacgttggt	gtggtatccc	ctcatggata	840
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cagaaatgaa	aatgggatac	ttaagaaatg	gatatacaaga	tttgatgtgt	ggccatatct	1140
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caaaaatact	gttggaacag	atgagagtca	tactgccttt	actctgcctg	gtctgtaccg	1500
agttgtccat	gggatcgatg	tcttcgatcc	aaagtccaat	atagtctctc	ctggagctga	1560
catgtccata	tactttccac	ataccgagaa	ggccaagcga	ctcacctctc	ttcatggttc	1620
aatcgaaaat	ttgatttatg	accgggagca	aaacgatgaa	cacattgggc	atctggatga	1680
ccggtcaaa	cccatcctct	tctccatggc	aagactcgac	aggggtgaaga	acataacagg	1740
gctggtcgaa	gcttttgcta	agtgcgctaa	gctgagggag	ctggtaaacc	ttgtcgtcgt	1800
tgccgggtac	aatgatgtca	acaagtccaa	ggacagggaa	gagatcgccg	agatagagaa	1860
gatgcatgaa	ctcatcaaga	cccacaactt	gttcgggcag	ttccgctgga	tctctgccca	1920
gacaaacagg	gcccgtaaag	gcgagctcta	tcgctacatc	gctgataccc	atggtgcttt	1980
cgtacagccg	gccttgtagt	aagcgttcgg	tctcacccgtc	gttgaggcca	tgacctgtgg	2040
gcttcctact	ttcgcgacgc	tccatggagg	tccagctgag	atcatagagc	atggcgctctc	2100
gggctttccac	attgacccgt	accaccccga	acaggctggt	aatctgatgg	ccgacttctt	2160
cgaccgggtg	aagcaagacc	cagatcactg	ggtgaatata	tctggagcag	ggctgcagcg	2220
catatacgag	aagtacacat	ggaagatata	ctcagagagg	ttgatgacac	tggccgggggt	2280
ctacggtttc	tggaagtacg	tgctgaagct	cgagaggctg	gagacgaggc	gctaccttga	2340
gatgtttctac	atactgaagt	tccgcgagct	ggcgaagacc	gtgccgcttg	caattgacca	2400
accgcagtag	cttgcgcaac	tgcgactgcg	tagcacttgg	tacaagactg	aaacctgaag	2460
gaccttcagt	aatttaggcg	cggcagacgg	tagccaataa	aatgtgcccg	agctgaactg	2520
gtttttttatt	atgtacataa	tggcagtata	acaaaattac	tgaaggcagg	tgggttgacg	2580
ttgtgtgttc	gttactgttt	actgtattat	gtcaagctgt	cggctgcaat	ttctttgctg	2640
gcaagccgca	ggcactggtg	aagtgtctgat	aaatacatca	tattctgttg	acctgtgaaa	2700
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	cggccgc			

Figure 11